



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/687,204
Source: 1 FWO
Date Processed by STIC: 10/18/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~
~~VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND~~
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/687,204

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading):
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 10-11, 13, 16 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/687,204

DATE: 10/18/2004

TIME: 13:54:11

Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\10182004\J687204.raw

4 <110> APPLICANT: Boehringer Ingelheim International GmbH
 6 <120> TITLE OF INVENTION: Composition for the Treatment of
 7 Infection by Flaviviridae Viruses
 10 <130> FILE REFERENCE: 13/118
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/687,204
 C--> 13 <141> CURRENT FILING DATE: 2003-10-16
 15 <150> PRIOR APPLICATION NUMBER: US 60/421,900
 16 <151> PRIOR FILING DATE: 2002-10-29
 18 <160> NUMBER OF SEQ ID NOS: 16
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 28
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Primer
 30 <400> SEQUENCE: 1
 31 ctccgatccg gcgcccacac cggcctac
 33 <210> SEQ ID NO: 2
 34 <211> LENGTH: 33
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Artificial Sequence
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: primer
 41 <400> SEQUENCE: 2
 42 ctctctagat cagcactctt ccatttcac gaa
 44 <210> SEQ ID NO: 3
 45 <211> LENGTH: 36
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Artificial Sequence
 49 <220> FEATURE:
 50 <223> OTHER INFORMATION: primer
 52 <400> SEQUENCE: 3
 53 ctctctagat cagcactctt ccatttcac gaactc
 55 <210> SEQ ID NO: 4
 56 <211> LENGTH: 34
 57 <212> TYPE: DNA
 58 <213> ORGANISM: Artificial Sequence
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: primer
 63 <400> SEQUENCE: 4
 64 ctccgatccg gcgcccacac cggcctactc ccaa
 66 <210> SEQ ID NO: 5

Does Not Comply
Corrected Diskette Needed

pr 2-3

28

33

36

34

RAW SEQUENCE LISTING

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Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\10182004\J687204.raw

67 <211> LENGTH: 16
 68 <212> TYPE: PRT
 69 <213> ORGANISM: HCV peptide *see item 10 on Euro Summary sheet*
 71 <400> SEQUENCE: 5
 72 Pro Asp Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu Cys
 73 1 5 10 15
 76 <210> SEQ ID NO: 6
 77 <211> LENGTH: 28
 78 <212> TYPE: DNA
 79 <213> ORGANISM: Artificial Sequence
 81 <220> FEATURE:
 82 <223> OTHER INFORMATION: primer
 84 <400> SEQUENCE: 6
 85 ctccggtccg gctccatta ctgcttac 28
 87 <210> SEQ ID NO: 7
 88 <211> LENGTH: 43
 89 <212> TYPE: DNA
 90 <213> ORGANISM: Artificial Sequence
 92 <220> FEATURE:
 93 <223> OTHER INFORMATION: primer
 95 <400> SEQUENCE: 7
 96 gacgcgtcga cgcggccgct cagcactctt ccattttcact gaa 43
 98 <210> SEQ ID NO: 8
 99 <211> LENGTH: 31
 100 <212> TYPE: DNA
 101 <213> ORGANISM: Artificial Sequence
 103 <220> FEATURE:
 104 <223> OTHER INFORMATION: primer
 106 <400> SEQUENCE: 8
 107 ctccggtccg gccccgatca cagcatatcg c 31
 109 <210> SEQ ID NO: 9
 110 <211> LENGTH: 41
 111 <212> TYPE: DNA
 112 <213> ORGANISM: Artificial Sequence
 114 <220> FEATURE:
 115 <223> OTHER INFORMATION: primer
 117 <400> SEQUENCE: 9
 118 caccgctcga gtcagcattc ttccatctca tcatattggt g 41
 120 <210> SEQ ID NO: 10
 121 <211> LENGTH: 11
 122 <212> TYPE: PRT
 123 <213> ORGANISM: Artificial Sequence *This needs explanation in 2207-2237 section (see item 11 on Euro Summary sheet)*
 125 <220> FEATURE:
 126 <223> OTHER INFORMATION: Asp at position 1 is linked to anthranilyl
 128 <223> OTHER INFORMATION: Xaa at position 6 is aminobutyric acid [C(O)-O]
 130 <223> OTHER INFORMATION: Xaa at position 9 is (3-nitro)tyrosine
 --> 132 <400> 10
 --> 133 Asp Asp Ile Val Pro Xaa Ala Met Xaa Thr Trp
 134 1 5 10

RAW SEQUENCE LISTING

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Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\10182004\J687204.raw

137 <210> SEQ ID NO: 11
138 <211> LENGTH: 11
139 <212> TYPE: PRT
140 <213> ORGANISM: Artificial Sequence *needs explanation - see item 11 on Error summary sheet*
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Xaa at position 6 is aminobutyric acid
145 <400> SEQUENCE: 11
-> 146 Asp Asp Ile Val Pro Xaa Ala Met Tyr Thr Trp
147 1 5 10
150 <210> SEQ ID NO: 12
151 <211> LENGTH: 12
152 <212> TYPE: PRT
153 <213> ORGANISM: HCV Peptide *see item 10 on Error summary sheet*
155 <400> SEQUENCE: 12
156 Asp Asp Ile Val Pro Cys Ser Met Ser Tyr Thr Trp
157 1 5 10
160 <210> SEQ ID NO: 13
161 <211> LENGTH: 11
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence *needs explanation - see item 11*
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Xaa is at position 1 is anthranilyl-Asp
168 <223> OTHER INFORMATION: Xaa at position 2 is (d)Glu
170 <223> OTHER INFORMATION: Xaa at position 6 is norvaline[C(O)-O]
172 <223> OTHER INFORMATION: Xaa at position 9 is (3-nitro)tyrosine
-> 174 <400> 13
-> 175 Xaa Xaa Ile Val Pro Xaa Ala Met Xaa Thr Trp
176 1 5 10
179 <210> SEQ ID NO: 14
180 <211> LENGTH: 30
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: primer
187 <400> SEQUENCE: 14
188 cgcataatggc accttttacg ctgcagtgtc 30
190 <210> SEQ ID NO: 15
191 <211> LENGTH: 33
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: primer
198 <400> SEQUENCE: 15
199 cgcgcgctcg agacactcct ccacgatttc ttc 33
201 <210> SEQ ID NO: 16
202 <211> LENGTH: 9
203 <212> TYPE: PRT
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:

RAW SEQUENCE LISTING

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Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\10182004\J687204.raw

207 <223> OTHER INFORMATION: Xaa at position 1 is acetylated-Asp
209 <223> OTHER INFORMATION: Xaa at position 3 is Asp (EDANS)
211 <223> OTHER INFORMATION: Xaa at position 6 is amino butyric acid [C(O)-O]
213 <223> OTHER INFORMATION: Xaa at position 9 is Lys[DABCYL]
-> 215 <400> 16
-> 216 Xaa Glu Xaa Glu Glu Xaa Ala Ser Xaa
217 1 5

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/687,204

DATE: 10/18/2004

TIME: 13:54:12

Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\10182004\J687204.raw

se of n's or Xaa's (NEW RULES):

se of n's and/or Xaa's have been detected in the Sequence Listing.

se of <220> to <223> is MANDATORY if n's or Xaa's are present.

n <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

eq#:10; Xaa Pos. 6,9
eq#:11; Xaa Pos. 6
eq#:13; Xaa Pos. 1,2,6,9
eq#:16; Xaa Pos. 1,3,6,9

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/687,204

DATE: 10/18/2004

TIME: 13:54:12

Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\10182004\J687204.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:132 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:133 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:10
L:133 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:146 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:11
L:146 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:11
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:174 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:175 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13
L:175 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:215 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:216 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:16
L:216 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:16
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0